

Run on:	March 17, 2003, 08:44:41 ; Search time 13 Seconds (without alignments) 2482.199 Million cell updates/sec														
OM protein - protein search, using sw model															
Title:	US-10-010-227-3														
Perfect score:	4055														
Sequence:	1 MFGAESTPQTLYDKVLUQAHV..... KAVPVPTINRGERKKEPLEW 778														
Scoring table:	BLOSUM62														
Database :	Gapext 10.0 , Gapext 0.5														
Searched:	112892 seqs, 41476328 residues														
Total number of hits satisfying chosen parameters:	112892														
Post-processing:	Minimum Match 0% Maximum Match 100% Listing first 100 summaries														
Minimum DB seq length:	0														
Maximum DB seq length:	200000000														
Result No.	Score	Query Match	Length	DB ID	Description										
1	2682.5	65.2	755	1	LEU2_RHPU										
2	2546	62.8	750	1	LEU2_RHINI										
3	2543	62.7	744	1	LEU2_RHML										
4	2492.5	62.7	733	1	LEU2_RUSTMA										
5	2473.5	61.0	758	1	LEU2_SCHPO										
6	2456.5	60.6	779	1	LEU2_YEAST										
7	2456.5	59.6	770	1	LEU2_CANMA										
8	2076	51.2	644	1	LEU2_RHIRA										
9	1636	40.3	469	1	LEU2_RHIME										
10	1611	39.7	469	1	LEU2_BRUME										
11	1584	39.1	469	1	LEU2_AGRITS										
12	1567.5	38.7	469	1	LEU2_RHILLO										
13	1562	38.5	479	1	LEU2_CAURC										
14	1548.5	38.2	469	1	LEU2_NIIMB										
15	1545.5	38.1	469	1	LEU2_NEIMA										
16	1522.5	37.5	479	1	LEU2_XANCP										
17	1514.5	37.3	479	1	LEU2_XANAC										
18	1507.5	37.2	474	1	LEU2_PBBAE										
19	1498.5	37.0	474	1	LEU2_XYLFA										
20	1493	36.8	469	1	LEU2_RALSO										
21	1483.5	36.6	465	1	LEU2_ECOLI										
22	1477.5	36.4	465	1	LEU2_SALTY										
23	1477.5	36.4	465	1	LEU2_SALTI										
24	1471	36.3	468	1	LEU2_HABIN										
25	1469.5	36.2	465	1	LEU2_ECO57										
26	1452	35.8	476	1	LEU2_YRPE										
27	1446.5	35.7	467	1	LEU2_PASMU										
28	1429	34.8	485	1	LEU2_ACTT1										
29	1413	34.8	471	1	LEU2_BUGAI										
30	1399	34.5	472	1	LEU2_BACHD										
31	1396	34.4	472	1	LEU2_BACILUS										
32	1393.5	34.4	472	1	LEU2_BACSU										
33	1385.5	34.2	476	1	LEU2_SIRCO										
SUMMARIES															
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.															
Copyright (c) 1993 - 2003 Compugen Ltd.															
GenCore version 5.1.4_P5_4578															
053237 mycobacteri															
085072 buchnera ap															
085065 buchnera ap															
033123 mycobacteri															
P58946 corynebacteri															
P48573 buchnera ap															
P58945 buchnera ap															
Q9p1wi campylobact															
031293 buchnera ap															
Q92a25 listeria in															
Q99s3 staphylococ															
Q9evi3 buchnera ap															
Q9evn4 buchnera ap															
Q9evi7 buchnera ap															
Q9evb0 buchnera ap															
Q9evi9 buchnera ap															
Q9evi5 buchnera ap															
Q9evi6 buchnera ap															
Q9evi7 pyrococcus															
Q9rtv7 methanopyru															
Q9rtv8 methanobact															
Q9rtv9 methanobact															
Q9rtv2 thermotilak															
Q9rtv3 thermotilak															
Q9rtv4 thermotilak															
Q9rtv5 thermotilak															
Q9rtv6 thermotilak															
Q9rtv7 thermotilak															
Q9rtv8 thermotilak															
Q9rtv9 thermotilak															
Q9rtv10 thermotilak															
Q9rtv11 thermotilak															
Q9rtv12 thermotilak															
Q9rtv13 thermotilak															
Q9rtv14 thermotilak															
Q9rtv15 thermotilak															
Q9rtv16 thermotilak															
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Q9rtv20 thermotilak															
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Q9rtv22 thermotilak															
Q9rtv23 thermotilak															
Q9rtv24 thermotilak															
Q9rtv25 thermotilak															
Q9rtv26 thermotilak															
Q9rtv27 thermotilak															
Q9rtv28 thermotilak															
Q9rtv29 thermotilak															
ALIGNMENTS															

LEU2_RHIPU	STANDARD;	PRT;	755 AA.
ID			
AC	P55215;		
DT	01-OCT-1995 (Rel. 34, Created)		
DT	01-OCT-1995 (Rel. 34, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	3-isopropylmaleate dehydratase (EC 4.2.1.33) (Isopropylmaleate isomerase) (Alpha-IPM isomerase) (IPMI).		
GN	LEU2		
OS	Rhizomucor pusillus		
OC	Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mucoraceae;		
CC	Rhizomucor		
CC	NCBI_TaxID=4840;		
RN	[1]		
RP	SEQUENCE FROM N. A.		
RA	PMID=96339000; PubMed=8766701;		
RA	Wada M., Beppu T., Horinouchi S.;		
RT	"Interrelative transformation of the zygomycete Rhizomucor pusillus by homologous recombination";		
RL	Appl. Microbiol. Biotechnol. 45:652-657 (1996).		
CC	-!- FUNCTION: Catalyzes the isomerization between 2-isopropylmaleate and 3-isopropylmaleate, via the formation of 2-isopropylmaleate.		
CC	-!- CATALYTIC ACTIVITY: 3-isopropylmaleate = 2-isopropylmaleate + H(2)O.		
CC	-!- CATALYTIC ACTIVITY: 2-isopropylmaleate + H(2)O = 2-isopropylmaleate.		
CC	-!- PATHWAY: Leucine biosynthesis; second step.		
CC	-!- SUBUNIT: Monomer (By similarity).		
CC	-!- SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY.		
CC	-----		
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CC	-----		
DR	D67033; BAA1052.1; -.		
DR	InterPro: IPR000573; Aconitase_C.		
DR	InterPro: IPR001030; Aconitase_N.		
DR	InterPro: IPR004431; LeuD.		
DR	InterPro: IPR00330; aconitase_1.		
DR	PFam: PF00654; Aconitase_C_1.		
DR	PRINTS: PR00415; ACONITASE.		
DR	ProDom: PD000511; Aconitase_N_1.		
DR	TIGRFAMS; TIGR00170; leuD_1.		
DR	PROSITE; PS00450; ACONITASE_1.		
DR	PROSITE; PS1244; ACONITASE_2.		
KW	Leucine biosynthesis; Lyase; Iron-sulfur; 4Fe-4S.		
FT	METAL 353 IRON-SULFUR (4Fe-4S) (BY SIMILARITY).		
FT	METAL 413 IRON-SULFUR (4Fe-4S) (BY SIMILARITY).		
FT	METAL 416 IRON-SULFUR (4Fe-4S) (BY SIMILARITY).		
SQ	SEQUENCE 755 AA; 82486 MW; [4E0537136BA6D11 CRC64];		
Query Match Similarity	66.2%;	Score	2692.5; Length 755;
Best Local Similarity	68.0%;	Pred. No.	1..3e-173;
Matches	527; Conservative	Mismatches	144; Indels
			27; Gaps
			12;
Qy	9 QTLYDKVLUQAHVYDEKLDTVLLYIDRHLVHEYTSPOAFGLNRAGRKVRPDTLATTD		68
Db	3 RTYLDKWDHVDQOBEGTCLYIDRHLVHEYTSPOAFGLNRAGRKVRPDTLATTD		62
Qy	69 HNPVPTISKALDIASTKEEDDSRTOCYTLEENYKEFQVYFGSLDKRQGYVHVGPGQ		128
Db	63 HNPPTPDKNFKQVNSTFQEDSRTOCTELHNVKERGTYFGMDSSQGIVVIGPGQ		122
Qy	129 FFLPGCTVNCGDSHTSTHGAFGALAFGIGTSEYEHVLAQCLTKRSKMRQYDGEAP		188
Db	123 FFLPGCTVNCGDSHTSTHGAFGALAFGIGTSEYEHVLAQCLTKRSKMRQYDGEAP		182

DR	InterPro; IPR00573; Aconitase_C.			
DR	InterPro; IPR001030; Aconitase_N.			
DR	InterPro; IPR004430; LeuC.			
DR	InterPro; IPR004431; LeuD.			
DR	Pfam; PF00694; Aconitase_C_1.			
DR	PRINTS; PR00415; ACONITASE.			
DR	ProDom; P000511; Aconitase_N_1.			
DR	TIGRFAMS; TIGR00170; leuC_1.			
DR	TIGRFAMS; TIGR00171; leuD_1.			
DR	PROSITE; PS00450; ACONITASE_1.			
DR	PROSITE; PS01244; ACONITASE_2_1.			
DR	Leucine biosynthesis; Lyase; Iron-sulfur; 4Fe-4S.			
FT	METAL_341_401_404; IRON-SULFUR (4Fe-4S).			
FT	METAL_401_404; IRON-SULFUR (4Fe-4S).			
FT	METAL_404; IRON-SULFUR (4Fe-4S).			
SEQUENCE	744 AA; 80833 MW; 9E5A330891D3745C CRC64;			
Query Match Score	62.7%; Score 2543; DB 1; Length 744;			
Best Local Similarity	66.1%; Pred. No. 3.4e-16;			
Matches 511; Conservative 68; Mismatches 160; Indels 34; Gaps 11;				
Qy	9 QTLQDKVLOAHVVDERKLDTVLYYDRHLVHEVTSPOAEGLNRAGKVKVRREPDCTLATTD 68			
Db	3 RTLYKQWDDHV-----DRHLVHEVTSPOAEGLNRAGKVKVRREPDCTLATVD 50			
Qy	69 HNVPTTSRKALKDIAFSKEDDSRTOCVTLEENVKEFGVTVYFGLSDKROGIVHVGPEQ 128			
Db	51 HNIPPTTRKFKSITTFIDEADSRQCTELTNVKEFELTYFGMENSROGLVHVGPEQ 110			
Qy	129 FTLPPTTVVGDSHSTHGFAGLAFGIGTSEVHVLATQCLITRSKSNMRQVQDGLAP 188			
Db	111 FTLPTTIVVGDSHSTHGFAGLAFGIGTSEVHVLATQCLITRSKSNMRQVQEGLTP 170			
Qy	189 GVSSKDVVVLHAIGIIGTAGGTGAVIEFCGSVIRSLSMSMEARMSICNMSIEGGRAGNMVAPD 248			
Db	171 GVTSDVAVHVGILGTAGETRCVBFCGSIAASMSMEARNSICNMSIEGGRAGNTAPD 230			
Qy	249 EITFPEYLKGRLPAPYKDSPEWMKATQYWKNLQSDGAKYDIDVFDIADKDVPTLWTGTP 308			
Db	231 EITFPEYLKGRLPAP-EGAELWDKAVQWKSLSKSDPNAKYDIDVKAASDIAPIITWTGTP 288			
Qy	309 EDVVFITGVVPDPDPEATEAKDADGRMLQVNGLAKAGTTPMDIPYDVKVFTGSPCTNRIED 368			
Db	289 QDVABITANVPDPSVSDPDKAAMERALEVIGLVPNTPLEEVKIDKAFIGSCTNRIED 348			
Qy	369 LRAAAVVKGRKAKPAPVKSAMVPPGSLVKTQABEGLDKIIFEEAGFEMWREAGCSMCLGM 428			
Db	349 LRSAAASIVKGKHAIWV-YAMVVPESGLVQRQABEGLDKVFTDGFDWREAGCSMCLGM 407			
Qy	429 NPDILAPQERCASSTNRNFEGQGGGRTHLSPMAAAGIVGLADVKLTDYKASPH 488			
Db	408 NPDQISPGERCASSTNRNFEGQGGGRTHLSPMAAAGIVGLADVKLTDYKASPH 467			
Qy	489 IAAQKSTVTKPHDVERI--NQDAHKDIIADIPEDNNGPHNTNTSASVGTSAGLKPFTIL 546			
Db	468 SPPPKFQT-QPKVYDEAAHKQAAQDAPVTDCCP--AGSPVNKGAPV-ASAMAAFTTL 522			
Qy	547 KGIAAPPLEKANVDTDAIIPQFELKIKRTSGNGLFYEMEFN-EDGTEKSDRVLNEKEPYR 605			
Db	523 KGIVAPLAISNVDTMIPKQFLKIKRTGIGSAFYGLDPAQAEKPDFLNQPAYR 582			
Qy	606 KASLIVCTGANFGCSSREHAPWALNDFGTSVIAFPSADIFFNNCFKNGMLPI-ILSQE 665			
Db	583 SSKLIVCTGPNGFCCSSREHAPWANDFGRCILTSFADIFFNNCFKNGMLPI-ILSQE 641			
Qy	666 QIAIIAAEARAGKEIIVDLEPNOLIKNATGETTCIEVEEFKRKHCLVNGLDDIGTQMED 725			
Db	642 QVDTLAKYATQAEIIVDLYHQK1RYPGEIPFDXMIIEBPRKHCLVNGLDDIGLNMQKDS 701			
Qy	726 KIAEFAKMTRETPWLDGTGTYLKERGOGKSLAAKAVPVPTNRRGEEKEPLEW 778			
Db	702 AIEKFEAKRTSTWMLDGRAY---KG-----KATKUTAIGSAQPAKEKLDW 744			
RESULT 4				
LEU2	USTMA	STANDARD;	PRT;	773 AA.
AC	P49501;			
DT	01-FEB-1996	(Rel. 33, Created)		
DT	01-FEB-1996	(Rel. 33, Last sequence update)		
DT	15-JUN-2002	(Rel. 41, Last annotation update)		
DE	3-isopropylmaleate dehydratase (EC 4.2.1.33) (Isopropylmalate isomerase) (Alpha-1PM isomerase) (IPMI).			
GN	LEU1;			
OS	Ustilago maydis (Smut fungus).			
OC	Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes; Ustilaginaceae; Ustilaginidae; Ustilaginales; Ustilaginaceae; Ustilago.			
NCBI_TaxID	5270;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=94171070; PubMed=8125330;			
RA	Rubin B. P. Li D. Holloman W. K.			
RT	"The LEU1 gene of <i>Ustilago maydis</i> ."			
Gene	140-131-135(1994).			
CC	-i- FUNCTION: Catalyzes the isomerization between 2-isopropylmaleate and 3-isopropylmaleate, via the formation of 2-isopropylmaleate.			
CC	-i- CATALYTIC ACTIVITY: 3-isopropylmalate = 2-isopropylmalate + H(2)O.			
CC	-i- CATALYTIC ACTIVITY: 2-isopropylmaleate + H(2)O = 2-isopropylmaleate.			
CC	-i- PATHWAY: Leucine biosynthesis; second step.			
CC	-i- SUBUNIT: Monomer (By similarity).			
CC	-i- SIMILARITY: BELONGS TO THE ACONITASE/1PM ISOMERASE FAMILY.			
CC	-----			
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CC	-----			
CC	EMBL; L20832; AAA44226_1; -			
DR	InterPro; IPR00573; Aconitase_C.			
DR	ProDom; P000511; Aconitase_N.			
DR	TIGRFAMS; TIGR00120; leuC_1.			
DR	InterPro; IPR004431; LeuD_1.			
PFam; PF003330; aconitase_1.				
PFam; PF00694; Aconitase_C_1.				
PRINTS; PR00415; Aconitase_E.				
DR	ProDom; P000511; Aconitase_N_1.			
DR	TIGRFAMS; TIGR00120; leuC_1.			
DR	InterPro; IPR004431; LeuD_1.			
DR	ProSite; PS01244; ACONITASE_2_1.			
KW	Leucine biosynthesis; lyase; Iron-sulfur; 4Fe-4S.			
FT	METAL_355_415_418; IRON-SULFUR (4Fe-4S).			
FT	METAL_415_418; IRON-SULFUR (4Fe-4S).			
SQ	SEQUENCE 773 AA; A936D8D1990DDC1 CRC64;			
Qy	-----			
Qy	Query Match Score 61.5%; Score 2492.5%; DB 1; Length 773; Best Local Similarity 64.0%; Pred. No. 9.4e-161; Indels 41; Gaps 9; Matches 488; Conservative 92; Mismatches 142; Gaps 41; Gaps 67.			
Db	3 PTKLYKEIFDFSHIVHEADGCLIYDHLVHEVTSPOAEGLNRAGKVRPDRDCTLATV 62			
Qy	-----			
Qy	68 DHNPVPTSRKALKDIAFSKEDDSRTOCVTLEENVKEFGVTVYFGLSDKRQGIVVHVGPEQ 127			
Db	63 DHNPVPTSRKSYRDTKSVETVDSRTOCVTLEENVKAFLGTFLSNRCGIVVHVGPEQ 122			
Qy	128 GFTLPGTTVVGDSHSTPFGAFLGTSPEVHLATQCLITKRSKMRQVGDGELA;			

123 GFTLPGATTIVCGDSHTSTHGAFGALAFGIGTSEVERVHLATOTLQKRAKNMLIQDGEIS 182
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Voelckel G., Aert R., Robben J., Gijmonprez B.,
 RA Weltjens I., Vanstreets E., Rieger M., Schaeffer M., Mueller-Auer S.,
 RA Cabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hubert H.,
 RA Borzym K., Dangler T., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
 RA Egger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Goux S., Lelauve V., Motterer S.,
 RA Callebaut F., Aves S.J., Kiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Usery D., Barrell B.G., Nurse P.,
 RT "The genome sequence of Schizosaccharomyces pombe,"
 RL Nature 415:871-880 (2002).
 -1- FUNCTION: Catalyzes the isomerization between 2-isopropylmalate
 and 3-isopropylmalate, via the formation of 2-isopropylmalate.
 -1- CATALYTIC ACTIVITY: 3-isopropylmalate = 2-isopropylmalate +
 H(2)O.
 CC CATALYTIC ACTIVITY: 2-isopropylmalate + H(2)O = 2-
 isopropylmalate.
 CC -1- PATHWAY: Leucine biosynthesis, second step.
 CC -1- SIMILARITY: BELONGS TO THE ACONITASE/1PM ISOMERASE FAMILY.
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 CC
 DR EMBL; Z99262.; CAB16402.1; -.
 DR InterPro; IPR00573.; Aconitase_C.
 DR InterPro; IPR001030.; Aconitase_N.
 DR InterPro; IPR004430.; LeuC.
 DR InterPro; IPR004331.; LeuD.
 DR Pfam; PF00330.; aconitase; 1.
 DR Pfam; PF00694.; Aconitase_C; 1.
 DR PRINTS; PR00415.; ACONITASE.
 DR ProdDom; PD000511.; Aconitase_N; 1.
 DR TIGRFAMs; TIGR00170.; leuC; 1.
 DR TIGRFAMs; TIGR00171.; leuD; 1.
 DR PROSITE; PS00450.; ACONITASE_1; 1.
 DR PROSITE; PS01244.; ACONITASE_2; 1.
 KW Leucine biosynthesis; Lyase; Iron-sulfur; 4Fe-4S.
 FT METAL 359 359 (BY SIMILARITY).
 FT METAL 420 420 (BY SIMILARITY).
 FT METAL 423 423 (BY SIMILARITY).
 SQ SEQUENCE 758 AA; 83782 MN; CE78C682888047 CRC64;
 Query Match 61.0%; Score 2473.5; -DB 1; Length 758;
 Best Local Similarity 62.9%; Pred. No. 1.8e-159;
 Matches 489; Conservative 92; Mismatches 172; Indels 25; Gaps 9;
 OC Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomyces; Schizosaccharomycetidae; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 RP [1] SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21048401; PubMed=11859360;
 RA Wood V., Gwillim R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collis M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
 RA Gerlès S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holloway S., Hornsby T., Howarth S., Huckle B.J., Hunt S., Jagele S.,
 RA Jones K., Jones L., Jones M., Leathem S., McDonald S., McLean D.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitzsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger S., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Voelckel G., Aert R., Robben J., Gijmonprez B.,
 RA Weltjens I., Vanstreets E., Rieger M., Schaeffer M., Mueller-Auer S.,
 RA Cabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hubert H.,
 RA Borzym K., Dangler T., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
 RA Egger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Goux S., Lelauve V., Motterer S.,
 RA Callebaut F., Aves S.J., Kiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Usery D., Barrell B.G., Nurse P.,
 RT "The genome sequence of Schizosaccharomyces pombe,"
 RL Nature 415:871-880 (2002).
 -1- FUNCTION: Catalyzes the isomerization between 2-isopropylmalate
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 H(2)O.
 CC CATALYTIC ACTIVITY: 2-isopropylmalate + H(2)O = 2-
 isopropylmalate.
 CC -1- PATHWAY: Leucine biosynthesis, second step.
 CC -1- SIMILARITY: BELONGS TO THE ACONITASE/1PM ISOMERASE FAMILY.
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 or send an email to license@isb-sib.ch).
 CC
 DR EMBL; Z99262.; CAB16402.1; -.
 DR InterPro; IPR00573.; Aconitase_C.
 DR InterPro; IPR001030.; Aconitase_N.
 DR InterPro; IPR004430.; LeuC.
 DR InterPro; IPR004331.; LeuD.
 DR Pfam; PF00330.; aconitase; 1.
 DR Pfam; PF00694.; Aconitase_C; 1.
 DR PRINTS; PR00415.; ACONITASE.
 DR ProdDom; PD000511.; Aconitase_N; 1.
 DR TIGRFAMs; TIGR00170.; leuC; 1.
 DR TIGRFAMs; TIGR00171.; leuD; 1.
 DR PROSITE; PS00450.; ACONITASE_1; 1.
 DR PROSITE; PS01244.; ACONITASE_2; 1.
 KW Leucine biosynthesis; Lyase; Iron-sulfur; 4Fe-4S.
 FT METAL 359 359 (BY SIMILARITY).
 FT METAL 420 420 (BY SIMILARITY).
 FT METAL 423 423 (BY SIMILARITY).
 SQ SEQUENCE 758 AA; 83782 MN; CE78C682888047 CRC64;
 Query Match 61.0%; Score 2473.5; -DB 1; Length 758;
 Best Local Similarity 62.9%; Pred. No. 1.8e-159;
 Matches 489; Conservative 92; Mismatches 172; Indels 25; Gaps 9;
 OC 1 MPGESTPOTLYKVLQHWDKLDGTVLYIRDRHLYHEVTPQAEGRLNRAGKVRP 60
 OC 1 MSPSVASPKTYLDPKVWHDVWLDQBDGTCILYDRHLYHEVTPQAEGRLNRAGKVRP 60
 OC 61 DCTVATDINPVTSKALKDASPIKEDDSRQTCVLTENKVERGTVYFLGLSDKRGIV 120
 OC 61 DCTVATDINPVTSKALKDASPIKEDDSRQTCVLTENKVERGTVYFLGLSDKRGIV 120
 DB 121 HVIGPEQFTLPGTIVCGDSHTSTHGAFGALFGIGTSEVERVHLATOCITKSNMRL 180
 DB 121 HVIGPEQFTLPGTIVCGDSHTSTHGAFGALFGIGTSEVERVHLATOCITKSNMRL 180
 OC 181 QVQGELAPVSSKQVWHAIGLITAGGTGAVIEFCGSVIRSLISMEAMSICNNISIEGA 240
 OC 181 RVNGKLUPIEGIASKDILHITIGVITAGGTGVSIFCGEAIEGLSMMEAMSMCNNSIEGA 240
 OC 241 RAGNVADEPTEFEYLGRPLAKPSDSPEWKATQYWKQIQLQSDPGAKYDIDVFDADI 300

Db	241	RAGMIAPDATTFEYVKNRPLAPKGD - DWEQAVAYWKTLSDENAKYDIEVEINAADVLP	298	
Qy	301	TLWGTSPSPDDVPTGWWPDPETPATEAKADGERMLQNGLKACTPMEIPVDKVFIGS	360	
Db	299	TWGTSPSPDVIPTGWWPDPETPATEAKADGERMLQNGLKACTPMEIPVDKVFIGS	358	
Qy	361	CTNSRIEDLRAAAAVVKGRKAKAPNPKSAMVPGSSLVKTQAAEGLDKLFEAEFFEWREA	420	
Db	359	CTNSRIEDLRAAAAVVKGRKAKAPNPKSAMVPGSSLVKTQAAEGLDKLFEAEFFEWREA	418	
Qy	421	GCSMCLGMNPDLQPERCSTSNSRNFEGRQGAGRTHLSPVMAAAAGIVGKLADEVRLK	480	
Db	419	GCSMCLGMNPDLQPERCSTSNSRNFEGRQGAGRTHLSPVMAAAAGIVGKLADEVRLK	478	
Qy	481	TDYKASPHIAYQKSTVTKPHDVERINQDAH--EKDIDADIPEPDNNPHPTNTASVGT	536	
Db	479	FG---DVSNGSPSITTKNPKDPSHDEVGDIGSVDDATDAVTDAGTATVAGSVSSG	533	
Qy	537	SAGLPKFTLKGIAAPLEKANVDTDALLPKQFLKTIKATRGLGNVALFYEMRNEDGTEKSD	596	
Db	534	SAGLPKFTLKGIAAPLEKANVDTDALLPKQFLKTIKATRGLGNVALFYEMRNEDGTEKSD	593	
Qy	597	FVNLKEPYRKASLIVCTGANFGCCSREHAPWALNDFGRSVIAPSFAFIFNSFKNM	656	
Db	594	FVNLKEPYRKASLIVCTGANFGCCSREHAPWALNDFGRSVIAPSFAFIFNSFKNM	652	
Qy	657	LPIPIKODAQEEAEEARAGKELEVDLNPQLTKNATCITCPEVEPRKHCLVNGLDD	716	
Db	653	LPIPIKODAQEEAEEARAGKELEVDLNPQLTKNATCITCPEVEPRKHCLVNGLDD	709	
Qy	717	IGLTMOMEDKIAFEAKMTRTPEMLDGTCYKLKGOGGKLAAKAVAVPPTNRGEEBKE	774	
Db	710	IGLTMOMEDKIAFEAKMTRTPEMLDGTCYKLKGOGGKLAAKAVAVPPTNRGEEBKE	777	
		RARLSPVKSINKQSSSRND	757	
RESULT 6				
	LEU2	YEAST	STANDARD;	PRT;
	ID	LEU2_YEAST		779 AA.
AC	PO264;			
DT	01-APR-1988	(Ref. 07, Created)		
DT	01-OCT-1996	(Ref. 34, Last sequence update)		
DT	15-JUN-2002	(Ref. 41, Last annotation update)		
DE	3-isopropylmalate dehydratase (EC 4.2.1.33)	(Isopropylmalate isomerase) (Alpha-IPM isomerase) (IPMI).		
DB	NCBI_TaxID=4932;			
RN	SEQUENCE FROM N.A.			
RC	STRAIN=L125-2B;			
RX	MEDLINE=91353082;	PubMed=1840714;		
RA	Skala J., Capieaux E., Balzi E., Chen W., Goffeau A.;			
RT	"Complete sequence of the <i>Saccharomyces cerevisiae</i> LEU1 gene encoding isopropylmalate isomerase.";			
RL	Yeast?	281-285 (1991).		
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Capieaux E., Balzi E., Chen W., Goffeau A.;			
RT	"Complete sequence of the <i>Saccharomyces cerevisiae</i> LEU1 gene encoding isopropylmalate isomerase.";			
RL	Yeast?	281-285 (1991).		
RN	[3]			
RP	SEQUENCE OF 1-48 FROM N.A.			
RX	MEDLINE=84162042;	PubMed=6323436;		
RA	Hsu Y.-P., Schimmel P. R.;			
RT	"yeast" LEU1. Expression of mRNA levels by leucine and relationship of 5'-noncoding region to that of LEU2.";			
RL	J. Biol. Chem. 259:3714-3719 (1984).			
RN	[4]			
RP	SEQUENCE OF 740-779 FROM N.A.			
RC	STRAIN=L125-2B;			
RX	MEDLINE=91353083;	PubMed=1882553;		
RA	Chen W., Capieaux E., Choder M., Goffeau A.;			
RESULT 7				
	LEU2	YEAST	STANDARD;	PRT;
	ID	LEU2_YEAST		779 AA.
AC	PO264;			
DT	01-APR-1988	(Ref. 07, Created)		
DT	01-OCT-1996	(Ref. 34, Last sequence update)		
DT	15-JUN-2002	(Ref. 41, Last annotation update)		
DE	3-isopropylmalate dehydratase (EC 4.2.1.33)	(Isopropylmalate isomerase) (Alpha-IPM isomerase) (IPMI).		
DB	NCBI_TaxID=4932;			
RN	SEQUENCE FROM N.A.			
RC	STRAIN=L125-2B;			
RX	MEDLINE=91353082;	PubMed=1840714;		
RA	Skala J., Capieaux E., Balzi E., Chen W., Goffeau A.;			
RT	"Complete sequence of the <i>Saccharomyces cerevisiae</i> LEU1 gene encoding isopropylmalate isomerase.";			
RL	Yeast?	281-285 (1991).		
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Hebling U., Hoffmann B., Delius H.;			
RL	Submitted (May-1996) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE OF 1-48 FROM N.A.			
RX	MEDLINE=84162042;	PubMed=6323436;		
RA	Hsu Y.-P., Schimmel P. R.;			
RT	"yeast" LEU1. Expression of mRNA levels by leucine and relationship of 5'-noncoding region to that of LEU2.";			
RL	J. Biol. Chem. 259:3714-3719 (1984).			
RN	[4]			
RP	SEQUENCE OF 740-779 FROM N.A.			
RC	STRAIN=L125-2B;			
RX	MEDLINE=91353083;	PubMed=1882553;		
RA	Chen W., Capieaux E., Choder M., Goffeau A.;			
RESULT 8				
	LEU2	YEAST	STANDARD;	PRT;
	ID	LEU2_YEAST		779 AA.
AC	PO264;			
DT	01-APR-1988	(Ref. 07, Created)		
DT	01-OCT-1996	(Ref. 34, Last sequence update)		
DT	15-JUN-2002	(Ref. 41, Last annotation update)		
DE	3-isopropylmalate dehydratase (EC 4.2.1.33)	(Isopropylmalate isomerase) (Alpha-IPM isomerase) (IPMI).		
DB	NCBI_TaxID=4932;			
RN	SEQUENCE FROM N.A.			
RC	STRAIN=L125-2B;			
RX	MEDLINE=91353082;	PubMed=1840714;		
RA	Skala J., Capieaux E., Balzi E., Chen W., Goffeau A.;			
RT	"Complete sequence of the <i>Saccharomyces cerevisiae</i> LEU1 gene encoding isopropylmalate isomerase.";			
RL	Yeast?	281-285 (1991).		
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Hebling U., Hoffmann B., Delius H.;			
RL	Submitted (May-1996) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE OF 1-48 FROM N.A.			
RX	MEDLINE=84162042;	PubMed=6323436;		
RA	Hsu Y.-P., Schimmel P. R.;			
RT	"yeast" LEU1. Expression of mRNA levels by leucine and relationship of 5'-noncoding region to that of LEU2.";			
RL	J. Biol. Chem. 259:3714-3719 (1984).			
RN	[4]			
RP	SEQUENCE OF 740-779 FROM N.A.			
RC	STRAIN=L125-2B;			
RX	MEDLINE=91353083;	PubMed=1882553;		
RA	Chen W., Capieaux E., Choder M., Goffeau A.;			
RESULT 9				
	LEU2	YEAST	STANDARD;	PRT;
	ID	LEU2_YEAST		779 AA.
AC	PO264;			
DT	01-APR-1988	(Ref. 07, Created)		
DT	01-OCT-1996	(Ref. 34, Last sequence update)		
DT	15-JUN-2002	(Ref. 41, Last annotation update)		
DE	3-isopropylmalate dehydratase (EC 4.2.1.33)	(Isopropylmalate isomerase) (Alpha-IPM isomerase) (IPMI).		
DB	NCBI_TaxID=4932;			
RN	SEQUENCE FROM N.A.			
RC	STRAIN=L125-2B;			
RX	MEDLINE=91353082;	PubMed=1840714;		
RA	Skala J., Capieaux E., Balzi E., Chen W., Goffeau A.;			
RT	"Complete sequence of the <i>Saccharomyces cerevisiae</i> LEU1 gene encoding isopropylmalate isomerase.";			
RL	Yeast?	281-285 (1991).		
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Hebling U., Hoffmann B., Delius H.;			
RL	Submitted (May-1996) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE OF 1-48 FROM N.A.			
RX	MEDLINE=84162042;	PubMed=6323436;		
RA	Hsu Y.-P., Schimmel P. R.;			
RT	"yeast" LEU1. Expression of mRNA levels by leucine and relationship of 5'-noncoding region to that of LEU2.";			
RL	J. Biol. Chem. 259:3714-3719 (1984).			
RN	[4]			
RP	SEQUENCE OF 740-779 FROM N.A.			
RC	STRAIN=L125-2B;			
RX	MEDLINE=91353083;	PubMed=1882553;		
RA	Chen W., Capieaux E., Choder M., Goffeau A.;			
RESULT 10				
	LEU2	YEAST	STANDARD;	PRT;
	ID	LEU2_YEAST		779 AA.
AC	PO264;			
DT	01-APR-1988	(Ref. 07, Created)		
DT	01-OCT-1996	(Ref. 34, Last sequence update)		
DT	15-JUN-2002	(Ref. 41, Last annotation update)		
DE	3-isopropylmalate dehydratase (EC 4.2.1.33)	(Isopropylmalate isomerase) (Alpha-IPM isomerase) (IPMI).		
DB	NCBI_TaxID=4932;			
RN	SEQUENCE FROM N.A.			
RC	STRAIN=L125-2B;			
RX	MEDLINE=91353082;	PubMed=1840714;		
RA	Skala J., Capieaux E., Balzi E., Chen W., Goffeau A.;			
RT	"Complete sequence of the <i>Saccharomyces cerevisiae</i> LEU1 gene encoding isopropylmalate isomerase.";			
RL	Yeast?	281-285 (1991).		
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Hebling U., Hoffmann B., Delius H.;			
RL	Submitted (May-1996) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE OF 1-48 FROM N.A.			
RX	MEDLINE=84162042;	PubMed=6323436;		
RA	Hsu Y.-P., Schimmel P. R.;			
RT	"yeast" LEU1. Expression of mRNA levels by leucine and relationship of 5'-noncoding region to that of LEU2.";			
RL	J. Biol. Chem. 259:3714-3719 (1984).			
RN	[4]			
RP	SEQUENCE OF 740-779 FROM N.A.			
RC	STRAIN=L125-2B;			
RX	MEDLINE=91353083;	PubMed=1882553;		
RA	Chen W., Capieaux E., Choder M., Goffeau A.;			
RESULT 11				
	LEU2	YEAST	STANDARD;	PRT;
	ID	LEU2_YEAST		779 AA.
AC	PO264;			
DT	01-APR-1988	(Ref. 07, Created)		
DT	01-OCT-1996	(Ref. 34, Last sequence update)		
DT	15-JUN-2002	(Ref. 41, Last annotation update)		
DE	3-isopropylmalate dehydratase (EC 4.2.1.33)	(Isopropylmalate isomerase) (Alpha-IPM isomerase) (IPMI).		
DB	NCBI_TaxID=4932;			
RN	SEQUENCE FROM N.A.			
RC	STRAIN=L125-2B;			
RX	MEDLINE=91353082;	PubMed=1840714;		
RA	Skala J., Capieaux E., Balzi E., Chen W., Goffeau A.;			
RT	"Complete sequence of the <i>Saccharomyces cerevisiae</i> LEU1 gene encoding isopropylmalate isomerase.";			
RL	Yeast?	281-285 (1991).		
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Hebling U., Hoffmann B., Delius H.;			
RL	Submitted (May-1996) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE OF 1-48 FROM N.A.			
RX	MEDLINE=84162042;	PubMed=6323436;		
RA	Hsu Y.-P., Schimmel P. R.;			
RT	"yeast" LEU1. Expression of mRNA levels by leucine and relationship of 5'-noncoding region to that of LEU2.";			
RL	J. Biol. Chem. 259:3714-3719 (1984).			
RN	[4]			
RP	SEQUENCE OF 740-779 FROM N.A.			
RC	STRAIN=L125-2B;			
RX	MEDLINE=91353083;	PubMed=1882553;		
RA	Chen W., Capieaux E., Choder M., Goffeau A.;			
RESULT 12				
	LEU2	YEAST	STANDARD;	PRT;
	ID	LEU2_YEAST		779 AA.
AC	PO264;			
DT	01-APR-1988	(Ref. 07, Created)		
DT	01-OCT-1996	(Ref. 34, Last sequence update)		
DT	15-JUN-2002	(Ref. 41, Last annotation update)		
DE	3-isopropylmalate dehydratase (EC 4.2.1.33)	(Isopropylmalate isomerase) (Alpha-IPM isomerase) (IPMI).		
DB	NCBI_TaxID=4932;			
RN	SEQUENCE FROM N.A.			
RC	STRAIN=L125-2B;			
RX	MEDLINE=91353082;	PubMed=1840714;		
RA	Skala J., Capieaux E., Balzi E., Chen W., Goffeau A.;			
RT	"Complete sequence of the <i>Saccharomyces cerevisiae</i> LEU1 gene encoding isopropylmalate isomerase.";			
RL	Yeast?	281-285 (1991).		
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Hebling U., Hoffmann B., Delius H.;			
RL	Submitted (May-1996) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE OF 1-48 FROM N.A.			
RX	MEDLINE=84162042;	PubMed=6323436;		
RA	Hsu Y.-P., Schimmel P. R.;			
RT	"yeast" LEU1. Expression of mRNA levels by leucine and relationship of 5'-noncoding region to that of LEU2.";			
RL	J. Biol. Chem. 259:3714-3719 (1984).			
RN	[4]			
RP	SEQUENCE OF 740-779 FROM N.A.			
RC	STRAIN=L125-2B;			
RX	MEDLINE=91353083;	PubMed=1882553;		
RA	Chen W., Capieaux E., Choder M., Goffeau A.;			
RESULT 13				
	LEU2	YEAST	STANDARD;	PRT;
	ID	LEU2_YEAST		779 AA.
AC	PO264;			
DT	01-APR-1988	(Ref. 07, Created)		
DT	01-OCT-1996	(Ref. 34, Last sequence update)		
DT	15-JUN-2002	(Ref. 41, Last annotation update)		
DE	3-isopropylmalate dehydratase (EC 4.2.1.33)	(Isopropylmalate isomerase) (Alpha-IPM isomerase) (IPMI).		
DB	NCBI_TaxID=4932;			
RN	SEQUENCE FROM N.A.			
RC	STRAIN=L125-2B;			
RX	MEDLINE=91353082;	PubMed=1840714;		
RA	Skala J., Capieaux E., Balzi E., Chen W., Goffeau A.;			
RT	"Complete sequence of the <i>Saccharomyces cerevisiae</i> LEU1 gene encoding isopropylmalate isomerase.";			
RL	Yeast?	281-285 (1991).		
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Hebling U., Hoffmann B., Delius H.;			
RL	Submitted (May-1996) to the EMBL/GenBank/DBJ databases.			

Db	710	RKHLCLYNGLDDIGLTLQKEETIYEAKRKKRKFSSLEG-----	GSKLK--PIKG 757	
Qy	766	TNRGEEKKEPKLEW	778	
Db	758	TKKSTIYGNKAQEW	770	
RESULT 8				
LEU2_RHIRA	LEU2_RHIRA	STANDARD;	PRT;	644 AA.
ID	LEU2_RHIRA			
AC	P17299	(Rel. 15, Created)		
DT	01-AUG-1990	(Rel. 15, Last sequence update)		
DT	15-JUN-2002	(Rel. 41, Last annotation update)		
DE	3-isopropylmalate dehydratase (EC 4.2.1.33) (Isopropylmalate isomerase) (Alpha-IPM isomerase) (IPMI).			
GN	Rhizomucor racemosus (Mucor circinelloides f. lusitanicus).			
OC	Rhizomucor; Fungi; Zygomycota; Zygomycetes; Mucorales; Mucoraceae;			
OC	MUCOR			
OX	NCBI_TAXID=4841;			
RN	[1]	SEQUENCE FROM N.A.		
RC	STRAIN=ATCC 12168;	PubMed=2693214;		
RN	MEDLINE=90128277;			
RA	Isabel M., Roncerio G., Jepsen L.P., Stroeman P., van Heeswijk R.;			
RT	"Characterization of a leuA gene and an ARS element from Mucor circinelloides".			
RT	RL 84:335-343(1989).			
CC	-!- FUNCTION: Catalyzes the isomerization between 2-isopropylmalate and 3-isopropylmalate, via the formation of 2-isopropylmalate.			
CC	-!- CATALYTIC ACTIVITY: 3-isopropylmalate = 2-isopropylmalate + H(2)O.			
CC	-!- CATALYTIC ACTIVITY: 2-isopropylmalate + H(2)O = 2-isopropylmalate.			
CC	-!- PATHWAY: Leucine biosynthesis; second step.			
CC	-!- SUBUNIT: Monomer.			
CC	-!- SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).			
CC	-----			
DR	PIR; J00160; J00160.			
DR	PIR; S26865; S26865.			
DR	InterPro; IPR00573; Aconitase_C.			
DR	InterPro; IPR001030; Aconitase_N.			
DR	InterPro; IPR004440; Leuc.			
DR	PF00330; aconitase_1.			
DR	PF00654; Aconitase_C_1.			
DR	PRINTS; PRO0415; ACONITASE.			
DR	ProDom; PD000511; Aconitase_N_1.			
DR	TIGREAMS; TIGR00170; leuc_1.			
DR	PROSITE; PS00450; ACONITASE_1.			
DR	PROSITE; PS01244; ACONITASE_2.			
KW	Leucine biosynthesis; Lyase; Iron-sulfur; 4Fe-4S.			
FT	METAL 400	IRON-SULFUR (4Fe-4S) (BY SIMILARITY).		
FT	METAL 460	IRON-SULFUR (4Fe-4S) (BY SIMILARITY).		
FT	METAL 463	IRON-SULFUR (4Fe-4S) (BY SIMILARITY).		
SQ	SEQUENCE 644 AA;	65939 MW,	087EC26518BD497E CRC64;	
Query Match	51.2%	Score 2076; DB 1; Length 644;		
Best Local Similarity	68.8%	Pred. No. 9.9e-133;		
Matches	407;	Mismatches 114; Gaps 6;		
Qy	10	TLYDKVLUQAHVYDEKLGTGTVLYIDRHLVHEVTSPOAEGLRNAGRKYRPRPDCTLATDDH	69	
RESULT 9				
LEU2_RHIME	LEU2_RHIME	STANDARD;	PRT;	469 AA.
ID	Q92L76; Q9EV53;			
AC				
DT	15-JUN-2002 (Rel. 41, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	3-isopropylmalate dehydratase Large subunit (EC 4.2.1.33)			
DE	(Isopropylmalate isomerase) (Alpha-IPM isomerase) (IPMI).			
GN	LEUC OR R03206 OR SMC03823.			
OS	Rhizobium meliloti (Sinorhizobium meliloti).			
OC	Rhizobacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;			
OC	Sinorhizobium; Sinorhizobium.			
NCBI_TaxID=382;				
RN	[1]	SEQUENCE FROM N.A.		
RN	NCBI_TaxID=382;			
RP	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
RX	MEDLINE=21396507; PubMed=11481430;			
RA	Capela D., Bariloy-Rubier F., Gouzy J., Bothé G., Ampe F., Batut J.,			
RA	Boisnard P., Becker A., Bouthy M., Cadieu E., Dreano S., Goux S.,			
RA	Gondre T., Goffeau A., Kahn D., Kiss E., Lelaurie V., Masuy D.,			
RA	Pohl T., Porteau D., Puehler A., Purnelle B., Ramsperger U.,			
RA	Renard C., Thebaud P., Vandembrou M., Weidner S., Calibert F.;			
RT	"Analysis of the chromosome sequence of the legume symbiont Sinorhizobium meliloti strain 1021."			
RT	Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882 (2001).			
RL	[2]			
RN	SEQUENCE OF 22-469 FROM N.A.			
RP	SEQUENCE OF 22-469 FROM N.A.			
RC	STRAIN=GR;			
RA	Sanjuan-Benilla J.M., Munoz S., Olivares J., Sanjuan J.;			
RA	"The Sinorhizobium meliloti leuA gene is essential for symbiosis."			
RT	Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.			
CC	-!- FUNCTION: Catalyzes the isomerization between 2-isopropylmalate and 3-isopropylmalate, via the formation of 2-isopropylmalate.			

Db	117	EQGTLPGNTIVCGDSHTSTHAGALAHIGTSEVERVATQTLQKAKNMLVRVDGK	176	CC -!- SUBUNIT: Heterodimer of leuc and leud (By similarity). CC -!- SIMILARITY: BELONGS TO THE ACONITASE/1PM_ISOMERASE FAMILY. LEUC 1 CC SUBFAMILY.
Qy	186	LAPVSSKDVLHAGIGTAGGTGAVIEFGSVIRSLSMEARNMSICNMIEGGARAGNV	245	CC --- CC This SWISS-PROT entry is copyright. It is produced through a collaboration CC between the Swiss Institute of Bioinformatics and the EMBL outstation - CC the European Bioinformatics Institute. There are no restrictions on its CC use by non-Profit institutions as long as its content is in no CC modified and this statement is not removed. Usage by and for commercial CC entities requires a license agreement (See http://www.isb-sib.ch/announce/ CC or send an email to license@isb-sib.ch). CC
Db	177	LPAGVTAIDVLATLIGEICTAGGTYVYAGEA1RSLSMEGRNTICNMIEGGARAGHJ	236	DR EMBL; AE009217; AAL43690_1; DR EMBL; AE00184; AAK8428_1; ALT INIT.
Qy	246	APEDEITYKLGRPLAKYD3PENHKAQWKLQSDPQAKYD3DVFIAKDI1P7LWNG	305	DR InterPro; IPR0001030; Aconitase_N.
Db	237	ADPDTTEYKLGRPLAKYD3PENHKAQWKLQSDPQAKYD3DVFIAKDI1P7LWNG	294	DR PF0004430; Aconitase_1.
Qy	306	TSPDWWPITGVYVDPETATEAKDGRMLQYNGLKACTPMDIPVQKFEGSCTNSR	365	DR P000511; Aconitase_N_1.
Db	295	SSPDVVSVTGVNPDDIAETKRAKWKRLDYNGLKFGTKTIDAVRVSCTNSR	354	DR TIGRFAMS; TIGR00170; leuc_C_1.
Qy	366	IEDLRAAAAVKGKPKKAPNPKSAMVVPGSSGLVKTQAEFFGDK1KFEEAGFWRAGCSCN	425	DR PROSITE; PS01450; ACONITASE_2; 1.
Db	355	IEDLRAAAAKVVEGKPKVAPTV-NAMIVPQGSSGLVKEQAEAGLHK1KFEEAGDWRPGCSCN	413	DR PROSITE; PS01244; ACONITASE_2; 1.
Qy	426	LGMPNDILAPQEQCASTSNRNFQCRQAGGRTLMSPMMAAAAGIVGKLAADR	478	DR KW Leucine biosynthesis: Lyase; Iron-sulfur; 4Fe-4S; Complete proteome.
Db	414	LAMDDDRLKPKGERCASTSNRNFQCRQAGGRTLMSPMMAAAAGIVGKLAADR	466	FT METAL 350 (BY SIMILARITY). FT METAL 410 (4Fe-4S) (BY SIMILARITY). FT METAL 413 (4Fe-4S) (BY SIMILARITY).
RESULT 11				SO SEQUENCE 469 AA; 51048 MW; F8EFF03D4610D39 CRC4; 1.
LEU2_AGR5				
ID	QBUBV9; PRT; 469 AA.			Query Match 39.1%; Score 1584; DB 1; Length 469;
AC				Best Local Similarity 65.4%; Pred. No. 1..e-99;
DT	15-JUN-2002 (Rel. 41, Created)			Matches 310; Conservative 52; Mismatches 104; Indels 8; Gaps 3;
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	3-isopropylmalate dehydratase large subunit (EC 4.2.1.33)			
DE	3-isopropylmalate isomerase (Alpha-1PM isomerase) (IPMI).			
DE	1Sopropylmalate isomerase (Alpha-1PM isomerase) (IPMI).			
GN	LEUC OR ATU2709 OR AGR C 4910.			
OS	Agrobacterium tumefaciens (strain C58 / ATCC 33970)			
OC	Proteobacteria; alpha subdivision; Rhizobiaceae group;			
OC	Rhizobiaceae; Rhizobium.			
OX	NCBI_TaxID=176299; NCBI_TaxID=176299;			
RN	SEQUENCE FROM N.A.			
RX	MEDLINE-21608550; PubMed=11743193;			Qy 126 EGQFTLPGTTVCGD9HTSTHAGALAFGAGTGTSEVEHVLATQCL1TKRSKNMRIQVDGE 185
RA	Wood D.W., Setubal J.C., Kaul R., Monks D.B., Kitajima J.P., Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L., Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovے D. Sr., Chapman P., Cleland C., Deatherage G., Gillett W., Grant C., Kutyavain T., Levy R., Li M.-J., McClelland E., Palmieri A., Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D., Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespin W., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Chumley F., Tingey S.V., Tomb J.-P., Gordon M.P., Olson M.V., Nester E.W.; "The genome of the natural genetic engineer Agrobacterium tumefaciens C58." Science 294: 2317-2323 (2001). [12]			Db 117 EGQFTLPGMTIVCGD9HTSTHAGALAHG1GTSEVEHVLATQTL1OKKAKNMLVRVDGK 176
RX	Medline:21608551; PubMed=11743194;			Qy 186 LAPGYSKDKVYLHAIGLIGIPIAGGTGPVIEFGSVINSLSMARMSCNMS1EGGAR1GMV 245
RA	Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Askenazi M., Halling C., Mullin L., Qurolo B., Goldman B. S., Cao Y., Askenazi M., Tarchouk O., Bpp A., Liu F., Houmeli K., Gordon J., Daudin M., Doughty D., Scott C., Lappas C., Marketz B., Wollan C., Allinger M., Doughty D., Tomb J.-P., Gordon J., Lomo C., Sear C., Strub G., Flanagan C., Crowell C., Gurson J., Cielo C., Slater S.; "Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58." Science 294:2323-2328 (2001).			Db 177 LPESTYPAKDTI1GEIGTAGGTGPVIEFGSVINSLSMARMSCNMT1EGGARAGLI 236
RA	Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Askenazi M., Halling C., Mullin L., Qurolo B., Goldman B. S., Cao Y., Askenazi M., Tarchouk O., Bpp A., Liu F., Houmeli K., Gordon J., Daudin M., Doughty D., Scott C., Lappas C., Marketz B., Wollan C., Allinger M., Doughty D., Tomb J.-P., Gordon J., Lomo C., Sear C., Strub G., Flanagan C., Crowell C., Gurson J., Cielo C., Slater S.; "Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58." Science 294:2323-2328 (2001).			Qy 246 ADPDTTEYKLGRPLAKYD3PENHKAQWKLQSDPQAKYD3DVFIAKDI1P7LWNG 305
RA	Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Askenazi M., Halling C., Mullin L., Qurolo B., Goldman B. S., Cao Y., Askenazi M., Tarchouk O., Bpp A., Liu F., Houmeli K., Gordon J., Daudin M., Doughty D., Scott C., Lappas C., Marketz B., Wollan C., Allinger M., Doughty D., Tomb J.-P., Gordon J., Lomo C., Sear C., Strub G., Flanagan C., Crowell C., Gurson J., Cielo C., Slater S.; "Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58." Science 294:2323-2328 (2001).			Db 237 ADPDTEDYKDKP2PKGETE--QAIATWKLTKLSDEGAHYDKV1TDAANLPPIVSWG 294
RA	Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Askenazi M., Halling C., Mullin L., Qurolo B., Goldman B. S., Cao Y., Askenazi M., Tarchouk O., Bpp A., Liu F., Houmeli K., Gordon J., Daudin M., Doughty D., Scott C., Lappas C., Marketz B., Wollan C., Allinger M., Doughty D., Tomb J.-P., Gordon J., Lomo C., Sear C., Strub G., Flanagan C., Crowell C., Gurson J., Cielo C., Slater S.; "Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58." Science 294:2323-2328 (2001).			Qy 306 TSPDWWPITGVYVDPETATEAKDGRMLQYNGLKACTPMDIPVQKFEGSCTNSR 365
RN	SEQUENCE FROM N.A.			Db 295 SSPEPDTSVEGIVPNDDIEBENKR1SKWRLDYM1KPGTRITDDAIDRVEIGSTCNGR 354
RX	Medline:21608551; PubMed=11743193;			Qy 366 IEDLRAAAAVKGKPKKAPNPKSAMVPGSGLVYKTOBEEGLDKEEAGFWEAGGCSMC 425
RA	Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Askenazi M., Halling C., Mullin L., Qurolo B., Goldman B. S., Cao Y., Askenazi M., Tarchouk O., Bpp A., Liu F., Houmeli K., Gordon J., Daudin M., Doughty D., Scott C., Lappas C., Marketz B., Wollan C., Allinger M., Doughty D., Tomb J.-P., Gordon J., Lomo C., Sear C., Strub G., Flanagan C., Crowell C., Gurson J., Cielo C., Slater S.; "Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58." Science 294:2323-2328 (2001).			Db 355 IEDLRAAAK1VDGKRAVASTV-SAMIVPGSGLVKEQKEKG1KFLDAGFENREPQGCSMC 413
CC	-!- FUNCTION: Catalyzes the isomerization between 2- <i>i</i> -isopropylmalate and 3- <i>i</i> -isopropylmalate, via the formation of 2- <i>i</i> -isopropylmaleate.			CC -!- CATALYTIC ACTIVITY: 3 <i>i</i> -isopropylmalate = 2- <i>i</i> -isopropylmaleate + H ₂ O
CC	H ₂ O.			CC -!- CATALYTIC ACTIVITY: 2- <i>i</i> -isopropylmalate + H ₂ O = 2- <i>i</i> -isopropylmaleate.
CC	isopropylmalate.			CC -!- PATHWAY: Leucine biosynthesis; second step.
CC				CC (Isopropylmalate isomerase) (Alpha-1PM isomerase) (IPMI).

FT METAL	415	415	IRON-SULFUR (4Fe-4S) (BY SIMILARITY).
FT METAL	418	418	IRON-SULFUR (4Fe-4S) (BY SIMILARITY).
SEQUENCE	479 AA;	50693 MN;	8E19EB931A251BFA CRC64;
Query Match	38.5%; Score 1562;	DB 1;	Length 479;
Best Local Similarity	64.4%;	Pred. No. 3	5e-98;
Matches 307; Conservative 53; Mismatches 105; Indels 12; Gaps 5;			
Qy 9 QTLYDKVLUQAHYDVEKLDGTVLIXYIDRLHVETSPQAEGLRNAGRKYVRRPDCTLATTD 68			
Db 4 KTLYDKLWDAYSE-AGGEALYDILHLINEVTPAAGLRAAGRKYVRRPDTRLAVAD 62			
Qy 69 HNVPPTTBRKALDIASFKEDDSSATCQVTELEENYKEFGTYFGVLSKROGIVHVTGPEQG 128			
Db 63 HNIPTEQALGVDA--VADEEARLQLKTLLARNVADNGEFFPMGDIRGIVHVTGPEQG 119			
Qy 129 FTLPGTRTVCGDSHTSTSAGFAGLAFAIGGTSEVHVLATOCLLTKRSKNMRIQYDGLELAP 188			
Db 120 RTQPGMPTIVCGDSHTSTSAGFAGLAFAIGGTSEVHVLATQTLRKAKNMLVRDQLP 179			
Qy 189 GYSSKDVLHAIIGIIGTAGGTGAVIEFCGSVIRSLMEARMSICMSISGARAGMVAPD 248			
Db 180 GVTGKDVALAVIGEIGTAGGTGIVIEFAGEATAGLSMEGRMLCNLNTGGAKAGLVAAPD 239			
Qy 249 EITFEYUQGRPLAKPDKDPSPEWHAQTYQXRNLDSPGAKYDIDVFDIAKDIVPTLTWGTSP 308			
Db 240 DKTFAVYQGKPAPK-GAADMALSHWKTFFDDEAVPDRTVVIDGSALVPMVTWGTSP 297			
Qy 309 EDVVPITGVVPPDPETATEAKKADGRMLQYMLKAGTPEMDIPVVDKVFTGSCNTNSRIED 368			
Db 298 BDVTPITGVPDDESFPTDKEAHAHRAIDYMGKIAQGPISEARIDVFTGSCNTNSRIED 357			
Qy 369 LRAAFAVVK---GRKKPAVNUKSAMVYPGSLVYKTOABEEGLDKTIEFAGFPEKREAGCS 423			
Db 358 MRAAAAVQEAFLHGRLVAPHYK-AMVYPGSLVKEAQEEGLDAIFKAAGFDREPGCS 416			
Qy 424 MCLGMNFDILAQERCASTSNRNFEGRGAGGTHLMSPVMAAAGTIVSKLADYRL 480			
Db 417 MCLAMNFDLAQERCASTSNRNFEGRGAGGTHLVSFAMAAAAGHLVDVRL 473			
RESULT 14			
LEU2 -NEIMB	STANDARD;	PRT;	469 AA.
SEQUENCE FROM N.A.			
STRAIN=MCS8 / Serogroup B;			
RC 09JZ15;			
MDLINE=20175755; Published=10710307;			
DT 15-JUN-2002 (Rel. 41, Created)			
DT 15-JUN-2002 (Rel. 41, Last sequence update)			
DE 3-isopropylmalate hydratase large subunit (EC 4.2.1.33)			
DN (Isopropylmalate isomerase) (Alpha-IPM isomerase) (IPMI).			
OS Neisseria meningitidis (serogroup B).			
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.			
NCBI_TaxID=491;			
OC			
RN [1]			
RP SEQUENCE FROM N.A.			
RC /			
RC 09JZ15;			
RC MELLINE=20175755; Published=10710307;			
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,			
RA Eisen J.A., Gwynn M.L., DeBoy R., Peterson J.D., Dodson R.J.,			
RA Nelson W.C., Salzberg S.L., White O., Fleischmann R.D., Doughtery B.A.,			
RA Haft D.H., Parkay A., Blair E., Citoon H., Clark E.B.,			
RA Mason T., Cicco A., Utterback T.R., Khouli H., Qin H., Vamathevan J.,			
RA Cotton M.D., Utterback T.R., Khouli H., Qin H., Vamathevan J.,			
RA Gill J., Scarlato V., Masiognani V., Pizza M., Grandi G., Sun L.,			
RA Smith H.O., Fraser C.M., Moxon E.R., Rappoli R., Venter J.C.,			
RA RT "Complete genome sequence of Neisseria meningitidis serogroup B strain MC58";			
RT Science 287:1809-1815(2000).			
RL -!- FUNCTION: catalyzes the isomerization between 2-isopropylmalate			
CC and 3-isopropylmalate, via the formation of 2-isopropylmalate.			
CC -!- CATALYTIC ACTIVITY: 3-isopropylmalate = 2-isopropylmalate + H(2)O.			
CC			
RESULT 15			
LEU2 -NEIMB			
ID LRU2 NEIMA			
AC QJU62			
DT 15-JUN-2002 (Rel. 41, Created)			
PR; 469 AA.			

QY	246	APDEITTEFYEKLKGRLPLAKPIDSPEWHKATQWKNLLOSSDPGAKYDIDVFDKDIVTLTG	305
QY	247	3-isopropylmaleate hydratase large subunit (EC 4.2.1.33)	306
QY	248	(Isopropylmaleate isomerase) (Alpha-IPM isomerase) (IPMI)	307
QY	249	Neisseria meningitidis (serogroup A)	308
QY	250	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria	309
QY	251	NCBI_TaxID=65699;	310
QY	252	SEQUENCE FROM N.A.	311
QY	253	STRAIN=22491 / Serogroup A / Serotype 4A;	312
QY	254	MEDLINE=2022556; PubMed=10761919;	313
QY	255	Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,	314
QY	256	Davies R.M., Morelli G., Basham D., Brown D., Chillingworth T.,	315
QY	257	Jagels K., Leather S., Moulé S., Mungall K., Quail M.A.,	316
QY	258	Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,	317
QY	259	Whitehead S., Spratt B.G., Barrell B.G.,	318
QY	260	"Complete DNA sequence of a serogroup A strain of <i>Neisseria</i>	319
QY	261	meningitidis 22491.";	320
QY	262	Nature 404:502-506 (2000).	321
QY	263	-!- FUNCTION: Catalyzes the isomerization between 2-isopropylmaleate and 3-isopropylmaleate, via the formation of 2-isopropylmaleate.	322
QY	264	-!- CATALYTIC ACTIVITY: 3-isopropylmaleate = 2-isopropylmaleate + H(2)O.	323
QY	265	-!- CATALYTIC ACTIVITY: 2-isopropylmaleate + H(2)O = 2-isopropylmaleate.	324
QY	266	-!- PATHWAY: Leucine biosynthesis; second step.	325
QY	267	-!- SUBUNIT: Heterodimer of leuC and leuD (BY SIMILARITY).	326
QY	268	-!- SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY. LEUC 1 SUBFAMILY.	327
QY	269	CC	328
QY	270	CC	329
QY	271	CC	330
QY	272	CC	331
QY	273	CC	332
QY	274	CC	333
QY	275	CC	334
QY	276	CC	335
QY	277	CC	336
QY	278	CC	337
QY	279	CC	338
QY	280	CC	339
QY	281	CC	340
QY	282	CC	341
QY	283	CC	342
QY	284	CC	343
QY	285	CC	344
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QY	287	CC	346
QY	288	CC	347
QY	289	CC	348
QY	290	CC	349
QY	291	CC	350
QY	292	CC	351
QY	293	CC	352
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QY	295	CC	354
QY	296	CC	355
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QY	347	CC	406
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QY	596	CC	655
QY	597	CC	656
QY	598	CC	657

RESULT 1B		Db
LEU2_PSEAE	STANDARD;	PRT; 474 AA.
ID - LEU2_PSEAE		
AC Q9H233;		
DT 15-JUN-2002 (Rel. 41, Created)		
DT 15-JUN-2002 (Rel. 41, Last sequence update)		
DE 3-isopropylmalate dehydratase large subunit (EC 4.2.1.33) (Isopropylmalate isomerase) (Alpha-IPM isomerase) (IPMI).		
DE LEUC OR PA3121.		
OS Pseudomonas aeruginosa.		
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;		
OC Pseudomonas.		
OX NCBI_TAXID=287;		
RP STRAIN=ATCC 15692.		
RC MEDLINE=2043737; PubMed=10984043;		
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hiltagle W.O., Kowalik D.J., Lagrou M., Garber R.I., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith A.J., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reiser J., Sauer M.H., Hancock R.E.W., Lory S., Olson M.V., RT "Complete genome sequence of <i>Pseudomonas aeruginosa</i> PAO1, an opportunistic pathogen.";		
RL Nature 406:959-964(2000);		
CC -1- FUNCTION: Catalyzes the isomerization between 2-isopropylmalate and 3-isopropylmalate, via the formation of 2-isopropylmalate.		
CC -1- CATALYTIC ACTIVITY: 3-isopropylmalate = 2-isopropylmalate + H(2)O.		
CC -1- CATALYTIC ACTIVITY: 2-isopropylmalate + H(2)O = 2- isopropylmalate.		
CC -1- PATHWAY: Leucine biosynthesis; second step.		
CC -1- SUBUNIT: Heterodimer of leuc and leuD (By similarity).		
CC -1- SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY.		
CC LEUC 1		
CC		
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CC EMBL: AE004736; AAG00509.1; -		
CC InterPro: IPR001030; Aconitase_N.		
CC IntePro: IPR004430; Leuc.		
CC Pfam: PF00330; aconitase_1.		
CC PRION; PR00415; ACONITASE.		
CC PRION; PR00511; Aconitase_N_1.		
CC TIGRFAMS; TIGR00170; leuC_1.		
DR PROSITE: PS00450; ACONITASE_1; 1.		
DR PS01244; ACONITASE_2; 1.		
DR Leucine biosynthesis; Lyase; Iron-sulfur; 4Fe-4S; Complete proteome.		
FT METAL 353 353 IRON-SULFUR (4Fe-4S) (BY SIMILARITY).		
FT METAL 414 414 IRON-SULFUR (4Fe-4S) (BY SIMILARITY).		
FT METAL 417 417 IRON-SULFUR (4Fe-4S) (BY SIMILARITY).		
SQ SEQUENCE 474 AA; 51042 MW; 7B4A0F6500C228EC CRC64;		
Query Match 37.2%; Score 1507.5; DB 1; Length 474; Best Local Similarity 62.5%; Pred. No. 1.6-94; Matches 295; Conservative 61; Mismatches 113; Indels 3; Gaps 2;		
QY 9 QTLVYKVQLAQWVDEKUDGTVLWVYIDRILVHEWTPQAFEGLRNAGRKRPRPDTLATTD 68		
QY 4 KTLVYKVQLAQWVDEKUDGTVLWVYIDRILVHEWTPQAFEGLRNAGRKRPRPDTLATTD 63		
QY 69 HNVFPTTSRKALKDIAFSKEDSRQCTQVTELENKVEFGTYFGLSKDQKGVHVIGPEQ 128		
RESULT 19		Db
LEU2_XYLF	STANDARD;	PRT; 474 AA.
ID - LEU2_XYLF		
AC QPAX0;		
DT 15-JUN-2002 (Rel. 41, Created)		
DT 15-JUN-2002 (Rel. 41, Last sequence update)		
DE 3-isopropylmalate dehydratase large subunit (EC 4.2.1.33) (Isopropylmalate isomerase) (Alpha-IPM isomerase) (IPMI).		
DE LEUC OR XP2375;		
OS <i>Xylella fastidiosa</i> .		
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;		
OC Xylella.		
OX NCBI_TAXID=2371;		
RP STRAIN=85C;		
RC MEDLINE=20365717; PubMed=10910347;		
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M., Alvaranga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S., Barrios M.H., Bonacorsi B.D., Bordim S., Bove J.M.M., Briones M.R.S., Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro M.D., Carrer H., Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M., Coutinho L.L., Cristofani M.M., Dias-Neto B., Docena C., E-Borry H., Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A., Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R., Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A., Ho P.L., Hohlsel J.D., Juncqueira M.L., Kemper E.L., Kojima J.P., Krieger J.E., Kuramae E.E., Laiget F., Lambais M.R., Leste L.C.C., Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A., Machado M.A., Madreia M.A.B.N., Madeira H.M.F., Marinho C.L., Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y., Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorelo C.B., Moon D.H., Nagai M., Nasconde A.L.T.O., Netto L.E.S., Nhami A., Jr., Nobreaga F.G., Nunes L.R., Oliveira M.A., Oliveira M.C., Oliveira R.C., Palmeiro D.A., Paris A., Peixoto B.R., Pereira G.A.G., Pereira H.A.Jr., Pesquero J.B., Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M., de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawaki H.E., da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A.Jr., da Silva J.R., Silveira F.G., Silveira M.L.Z., Siqueira W.J., de Souza A.A., de Souza A.P., Trenzzi M.F., Truffi D., Tsai S.M., Tsukahara M.H., Valiada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L., Zogo M.A., Zatz M., Meidanis J., Setubal J.C.; RT "The genome sequence of the plant pathogen <i>Xylella fastidiosa</i> ."; RL Nature 406:151-159(2000);		

-	-	FUNCTION: Catalyzes the isomerization between 2-isopropylmaleate and 3-isopropylmaleate, via the formation of 2-isopropylmaleate.
-	-	CATALYTIC ACTIVITY: 3-isopropylmaleate = 2-isopropylmaleate + H ₂ O.
-	-	CATALYTIC ACTIVITY: 2-isopropylmaleate; second step.
-	-	BATHWAY: Leucine biosynthesis; second step.
-	-	SUBUNIT: Heterodimer of leuD and leuD (BY SIMILARITY).
-	-	SIMILARITY: BELONGS TO THE ACONITASE/1PM ISOMERASE FAMILY. LEUC 1 SUBFAMILY.
CC	CC	CC
CC	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	CC	CC
DR	DR	EMBL: AE004047; AAF85174; 1; -
DR	DR	InterPro: IPR01030; Aconitase_N.
DR	DR	InterPro: IPR004430; Leuc.
DR	DR	Pfam: PF000330; aconitase_1.
DR	DR	PRINTS: PR00415; ACONITASE.
DR	DR	ProDom: PD00051; Aconitase_N; 1.
DR	DR	TIGRFAMS: TIGR00170; leuc.
DR	DR	PROSITE: PS00450; ACONITASE_1.
DR	DR	PROSITE: PS01244; ACONITASE_2; 1.
KW	Leucine biosynthesis; Lyase; Iron-sulfur; 4Fe-4S; Complete proteome.	
FT	IRON-SULFUR (4Fe-4S) (BY SIMILARITY).	
FT	IRON-SULFUR (4Fe-4S) (BY SIMILARITY).	
FT	IRON-SULFUR (4Fe-4S) (BY SIMILARITY).	
FT	IRON-SULFUR (4Fe-4S) (BY SIMILARITY).	
SEQUENCE	474 AA;	99855DF82B23750 CRC64;
Query Match	37.0%	Score 1498.5; Length 474;
Best Local Similarity	63.1%	Pred. No. 6/re-94; Indels 3; Gaps 2;
Matches 298; Conservative 52; Mis matches 119;		
Qy	9	QTLYDKVLUQAHVVDKLDGTVLILYIDHHLHVTSPQAPEGLRNAGKVRPPDCTLATTD
Db	4	KTLYSLWLDTHEVARDDGSSIIYIDHHLHVTSPQAPEGLRAGPLWRNANIAJTPD
Qy	69	HNVPTTSRKALDIASFKEEDDSRTOCVTLDEBNVKERGTVYFGLSDKRGQIVHVGPGQ
Db	64	HNVPTTKAERQGSSLIS-IADTVSRLQVOTLDNCDDGIFEFKMDVYDQGIVHVGPGQ
Qy	129	FTLPGTTVCCGDSHTSHTGARGALAFGIGTSVEVHILATOCILTKRSKNNRICOVDGELAP
Db	123	ATLPGMTVCCGDSHTSHTGARGALARGTSVEVHILATOCILTKRSKNNRICOVDGELAP
Qy	189	GVSSKDVVVLHAIGIIGTAGGCAVIEFGSVIRSLSMEARMSLICNMSTEGGARAGMYAPD
Db	183	GVTARDIVLALIGKGTAGGNGYAVFESGSTIRALSMNEGRTICNMATEAGARVGMYAVD
Qy	249	BITFEYLKGRLPALKYDPSPEWKAQTOYWNKLQNSDPGKAYDIDVFDIADKDIVPPLTWGTS
Db	243	EKTQIVHGRPPAKP -GSDWDAAVAFWRGLVSDPDAHDFRIVVLSAEIJKPQVWTGTS
Qy	309	EDVVPITGVVYDPPETATEAKKADGRMLQYNGLKGATGTPMEDI1PVDVKFIGSCTNSRIED
Db	301	EMVSAVQDSVPPDPERETDPVKKESLITALKINGLQPNPDTITSKLDRYFIGSCTNSRIED
Qy	369	LRAAAVYVKGRKKRPPKSAVVPGLVKTQAEEGLKDIFBEGAFPWRREAGCSMCLGM
Db	361	LRAAAEVVKGRKVASTVYKQAVVVPGLSILVKAQAEVEGLDIFKTEAGFWREPGCSMCLAM
Qy	429	NPDILAPQERCCASTSNRNFEGRQGAGGRTHLMSPVAAAAGIVGKLAQYKRL
Db	421	NPDKLGSSEHCASTSNRNFEGRQGIGRTHLYSPAAAAYAVAGHFVDRREM

QY 189 GVSSKDVVLAHGIGTAGTGTGAVIEFCGSVIRSLSMARMSCINNSIEGARAGNAPD 248
 RC STRAIN=K12 / EMG2;
 RC MEDLINE=97143975; PubMed=9298646;
 RX
 RA Link A.-J., Robison K., Church G.M.;
 RT "Comparing the predicted and observed properties of proteins encoded
 in the genome of Escherichia coli K-12.";
 RL Electrophoresis 18:1259-1313 (1997).
 CC -- FUNCTION: Catalyzes the isomerization between 2-isopropylmalate
 and 3-isopropylmalate, via the formation of 2-isopropylmalate.
 CC -1 CATALYTIC ACTIVITY: 3-isopropylmalate = 2-isopropylmalate +
 H(2)O.
 CC -1 CATALYTIC ACTIVITY: 2-isopropylmalate + H(2)O = 2-
 isopropylmalate.
 CC -1 PATHWAY: Leucine biosynthesis; second step.
 CC -- SUBUNIT: Heterodimer of leuC and leuD.
 CC -1 SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY. LEUC 1
 SUBFAMILY.

Db 237 DITTEYIKRPLAPKXDSPPWKAQTYWQKQIQLSDPGAKYIDVFDAAKDVPTLTWGTSP 308
 QY 309 EDVPIRTGVPDPFATEAAKKADERRMLQYMLKGKAGTPMIDPVKVFQSCNTNRIED 368
 Db 295 EMVISIEDRVPDPKEKDPYKRNAMERALEMALONVAICDIRDKVFIGSCNTNRIED 354
 QY 369 LRAAAVVK-GRKKAPNPKSAMVPGSLVKTQAEELDKIFEEAGFENREAGCSMCL 426
 Db 355 MRAAWWVVKLGKRTIASNVLAMVPGSLVKEQAREGLDKIFKAAGFENREPGCSMCL 414
 QY 427 GMNDILAPQERCASTSNRNPEGROGAGGRTHLMSPVMAAAGIVGKADYRL 480
 Db 415 AMNADLIEPGERCASTSNRNPEGROGAGGRTHLVSAMAAAGALEGHFFVDVRL 468

RESULT 21

LEUD_ECOLI STANDARD; PRT; 465 AA.

ID LEUD_ECOLI STANDARD; PRT; 465 AA.

AC P30127; P78042;
 AC P30127; P78042; (Rel. 25, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 3-Bisopropylmalate dehydrogenase large subunit (EC 4.2.1.33)
 DE (Isopropylmalate isomerase) (Alpha-IPM isomerase) (IPMI).
 DE LEUC OR B0072;
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia;
 OC NCB-I_TaxID=562;
 RN [1] SEQUENCE FROM N.A.
 RP MEDLINE=91088346; PubMed=2124684;
 RA Rosenthal E.R., Calvo J.M.;
 RT "Apidicolin inhibits DNA polymerase II of Escherichia coli, an
 alpha-like DNA polymerase." Nucleic Acids Res. 18:7185-7186(1990).
 RL TIGR00170; leuC.
 RN SEQUENCE FROM N.A.
 RP STRAIN=K12;
 RC MEDLINE=92334977; PubMed=1630901;
 RA Yura T., Mori H., Nagai H., Nagata T., Ishihama A., Fujita N.,
 RA Isomo K., Mizobuchi K., Nakata A.;
 RT "Systematic sequencing of the Escherichia coli genome: analysis of
 the 0-2.4 min region." Nucleic Acids Res. 20:3305-3308(1992).
 RL SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=97426167; PubMed=9278503;
 RA Blattner R.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12." Science 277:1453-1474(1997).
 RL SEQUENCE OF 1-203 FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=91164169; PubMed=8119295;
 RA Kirino H., Aoki M., Hayashi Y., Ohba M., Yamagishi A., Wakagi T.,
 RA Oshimi T.;
 RT "Hydrophobic interaction at the subunit interface contributes to the
 thermostability of 3-isopropylmalate dehydrogenase from an extreme
 thermophile, Thermus thermophilus." Bur. J. Biochem. 220:275-281(1994).
 RL [5]

RP SEQUENCE OF 1-12.

RC STRAIN=K12 / EMG2;
 RC MEDLINE=97143975; PubMed=9298646;
 RX
 RA Link A.-J., Robison K., Church G.M.;
 RT "Comparing the predicted and observed properties of proteins encoded
 in the genome of Escherichia coli K-12.";
 RL Electrophoresis 18:1259-1313 (1997).
 CC -- FUNCTION: Catalyzes the isomerization between 2-isopropylmalate
 and 3-isopropylmalate, via the formation of 2-isopropylmalate.
 CC -1 CATALYTIC ACTIVITY: 3-isopropylmalate = 2-isopropylmalate +
 H(2)O.
 CC -1 CATALYTIC ACTIVITY: 2-isopropylmalate + H(2)O = 2-
 isopropylmalate.
 CC -1 PATHWAY: Leucine biosynthesis; second step.
 CC -- SUBUNIT: Heterodimer of leuC and leuD.
 CC -1 SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY. LEUC 1
 SUBFAMILY.

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 entities requires a license agreement. (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

CC DR EMBL; D17632; BAA21005.1; --.

CC DR EMBL; D10483; BAB9641.1; --.

CC DR EMBL; AEC00117; AAC73183.1; --.

CC DR EMBL; D17631; BAA21004.1; --.

CC DR SWISS-2DPAGE; P30127; ColI.

CC DR Ecogene; EG11576; leuC.

CC DR InterPro; IPR00130; Aconitase_N.

CC DR InterPro; IPR00430; Leuc.

CC DR Pfam; PF00330; aconitase_1.

CC DR PRINTS; PR0415; ACONITASE.

CC DR PRODOM; PD00051; Aconitase_N; 1.

CC DR TIGRFAMS; TIGR00170; leuC; 1.

CC DR PROSITE; PS00450; ACONITASE_1; 1.

CC DR PROSITE; PS0244; ACONITASE_2; 1.

CC KW Leucine biosynthesis; lyase; Iron-sulfur; 4Fe-4S; Complete proteome.

FT INIT_MET 0

FT METAL 346 346 IRON-SULFUR (4Fe-4S) (BY SIMILARITY).

FT METAL 406 406 IRON-SULFUR (4Fe-4S) (BY SIMILARITY).

FT METAL 409 409 IRON-SULFUR (4Fe-4S) (BY SIMILARITY).

FT CONFLICT 70 70 D -> G (IN REF. 1 AND 2).

FT CONFLICT 73 73 A -> G (IN REF. 4).

FT CONFLICT 270 270 MISSING (IN REF. 1).

FT CONFLICT 451 453 MISSING (IN REF. 1).

FT SEQUENCE 465 AA; 49778 MW; 0DC085F17FE89B16A CRC64;

QY 9 QTLQYKVLAHHWVKLQDGTWVLLKIDRHLVHEVTSPOAEGCIRNAGKVRPPDCTLATTQD 68
 Db 2 KTLYEKLFDAAHVVEAENETPLLYDTRHLVHEVTSPOAEGCIRHGRPVROGKTFATMD 61

QY 69 HNVFPTTSRALKDQDASFIKEDDSRQCVTLEENKEFGVYFGSDKROGVHVGPEQ 128
 Db 62 HNVVSTQD---KDINAC- GEMAR- GEMAR- GEMAR- GEMAR- GEMAR- GEMAR- 115

QY 129 FTLPGTTVVGDSHTSTHGAFFGAAGFTGTSSEVNLATOCITKESKNRQIQVDSLAP 188
 Db 116 VTLQPMTIVGDSHTATHGAFFGAAGFTGTSSEVNLATOCITKESKNRQIQVDSLAP 175

QY 189 GVSSKDVVLAHGIGTAGTGTGAVIEFCGSVIRSLSMARMSCINNSIEGARAGNAPD 248
 RA [1];
 RT "Hydrophobic interaction at the subunit interface contributes to the
 thermostability of 3-isopropylmalate dehydrogenase from an extreme
 thermophile, Thermus thermophilus." Bur. J. Biochem. 220:275-281(1994).
 RL [5]

QY 176 GITAKDIVLAIIGKTSAGGTGHVVEFCGEAIRDLMSMEGRWTLCINNAIEMGAKAGLVAPD 235

QY 249 EITTEYIKRPLAPKXDSPPWKAQTYWQKQIQLSDPGAKYIDVFDAAKDVPTLTWGTSP 308

Db	236	ETTFNYVKGRLLHAPK- -GKDFDDAVAYWKLQLQTDEGATFFDTVVTLQAEELISPQVTTWGTNP	293	DR InterPro; IPR004430; LeuC. PFam; PF00330; aconitase; 1.
Qy	309	EDVPIITGVDPDIPDVKVFGSCTNSRIED	368	DR TIGRFAMS; TIGR00170; LeuC; 1.
Db	294	GQVISVNDNIPDPAFFPVERASEAALKAYMGKXPKIPEAIDKVFJGSCTNSRIED	353	DR PROSITE; PS00450; ACONITASE; 1.
Qy	369	LRAAAAVYVKGRKKAPVNVKAMMVPGSGLYVKTQABREGDJKIFEEAGFEAEAGCSMCLGM	428	DR PROSITE; PS01244; ACONITASE; 2.
Db	354	LRAAAEIVVKGRKVAFGVQ- ALVVPGSGPVKAQAEAGLDKIFIEAGFEVNLPGCSMCLAM	412	KW Leucine biosynthesis; Lyase; Iron-sulfur; 4Fe-4S; Complete proteome.
Qy	429	NPDLAQPERCASTSNRNPFEGQAGGRTLMSPMVAAAGIVGKLADEVKL	480	FT INIT MET 0 BY SIMILARITY.
Db	413	NNDRINPGERCASTSNRNPFEGQGRGRTLVSFAMAALAVTGHFADIRNI	464	FT METAL 346 BY SIMILARITY.
RESULT 22				
ID	LE21_SALTY	STANDARD;	PRT;	465 AA.
AC	P15717;			
DT	01-APR-1990	(Rel. 14, Created)		
DT	15-JUN-2002	(Rel. 41, Last sequence update)		Score 36.4%; Length 465;
DE	3-isopropylmalate dehydratase large subunit 1 (EC 4.2.1.33)			Best Local Similarity 61.7%;
DE	(Isopropylmalate isomerase 1) (Alpha-IPM isomerase 1) (IPMI 1).			Matches 291; Conservative 63; Gaps 4;
GN	LEUC OR LEUC OR STM0111.			
OS	Salmonella typhimurium.			
OC	Salmonella; Proteobacteria; gamma subdivision; Enterobacteriaceae;			
OC	Salmonella.			
NCBI_TaxID	602;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=L-T2;			
RX	Medline=10272436; PubMed=2190189;			
RA	Rosenthal, E.R.; Calvo, J.M.;			
RT	"The nucleotide sequence of leuC from <i>Salmonella typhimurium</i> ."			
RL	Nucleic Acids Res. 18:3072-3072 (1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=L-T2 / SGSG1412 / ATCC 700720;			
RX	Medline=21531948; Pubmed=11677609;			
RA	McClelland, M.; Sanderson, K.E.; Spiech, J.; Clifton, S.W.; Latreille, P.;			
RA	Courtney, L.; Porwollik, S.; Ali, J.; Dante, M.; Hou, F.; Layman, D.;			
RA	Leonard, S.; Nguyen, C.; Scott, K.; Holmes, A.; Grewal, N.; Mulvaney, E.;			
RA	Ryan, E.; Sun, H.; Florea, L.; Miller, W.; Stoneking, T.; Nhan, M.;			
RA	Waterson, R.; Wilton, R.K.;			
RT	"Complete genome sequence of <i>Salmonella enterica</i> serovar <i>Typhimurium</i> L-T2."			
RL	Nature 413:852-855 (2001).			
CC	-I- FUNCTION: Catalyzes the isomerization between 2-isopropylmalate and 3-isopropylmalate, via the formation of 2-isopropylmalate.			
CC	-I- CATALYTIC ACTIVITY: 3-isopropylmalate = 2-isopropylmalate + H ₂ O.			
CC	-I- CATALYTIC ACTIVITY: 2-isopropylmalate + H ₂ O = 2-isopropylmalate.			
CC	-I- PATHWAY: Leucine biosynthesis; second step.			
CC	-I- SUBUNIT: Heterodimer of leuC and leuD (By similarity).			
CC	-I- SUBUNIT: BELONGS TO THE ACONITASE/IM ISOMERASE FAMILY. LEUC 1 SUBFAMILY.			
CC	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			RESULT 23
DR	X51476; CAA35840 1;			LEU2_SALTI
DR	EMBL; M31047; AAA21551; -.			STANDARD;
DR	EMBL; AE008639; AAL19075; 1; -.			FRT;
DR	PIR; S10171; S10171.			465 AA.
DR	StyGene; SG10197; leuC1.			
DR	InterPro; IPR001030; Aconitase_N.			
CC	DR EMBL; M31047; AAA21551; -.			OS Salmonella typhi.
CC	DR EMBL; AE008639; AAL19075; 1; -.			OC
CC	DR PIR; S10171; S10171.			OC
CC	DR StyGene; SG10197; leuC1.			NCBI_TaxID-601;
CC	DR InterPro; IPR001030; Aconitase_N.			[1]
RP	SEQUENCE FROM N.A.			

FT	METAL	407	407	IRON-SULFUR (4FE-4S) (BY SIMILARITY)	2;
FT	METAL	410	410	IRON-SULFUR (4FE-4S) (BY SIMILARITY)	
SEQ	SEQUENCE	468 AA;	50743 MW;	OF6AFAR97AAAE9F6 CRC64;	
Qy	Query	Match	36.3%;	Score 1471; DB 1; Length 468;	
Best Local Matches	Best Local Similarity	59.4%;	Pred. No. 4	7.692;	Gaps
Matches	Conservative	72;	Mismatches	112;	Indels
281;					
Qy	9	QTYDKVLYQAHVYDEKLGDGTWLLYIDRHLVHEVTSPQAEGFLRNAGRKVRRPDTCLATTED	68		
Db	2	KTYEKLFDSHIYEAEGETPILYINRHLIHEVTSPQAEGFLRVANRQTVNKTGFMID	61		
Qy	69	HNVPTTSRKALKDIASTFKEDDSRTQCVTLBEENYKEFGTYFPGLSIDRQGIVHVGPGC	128		
Db	62	HS1STQVRDVNK-----LEGQKIQVLELDKNTKATGKLFDTTKECGIVHVGPG	115		
Qy	129	FTLPGTTVCGDSHTSHTGAGAIAFGCTSEYEHVLTATQCLTKRSKMMRIOVGDGA	188		
Db	116	LTLPGMTIVCGDSHTATHGAGAIAFGCTSEYEHVLTATQLKOARAKSMKIEVGRKVS	175		
Qy	189	GVSSKDVVVHAIGIIGTAGGTGAVIEFOGGSVIRSLSMARMSCNMSSIEGGRAGAMVAPD	248		
Db	176	GITAKDITLAIICKTMAGGTGHVVEFCCEBAIQDLSMEGRMTVNAITEMGAKGLIADD	235		
Qy	249	ETTFEYLKGRRPLAKYDPEWHKATQYKWNLQSDPGAKYDIDVFDAKDIVPILTWGSP	308		
Db	236	ETTFAYLKDRPHAPK--GKDWEAVYVTKLSDDDAQDTVYTLREAKIAPOVTVWGNTP	293		
Qy	309	EDVYPICTGVVPDPETFATEAKDGRRMQYMGKRAGMTEDLPVDKVPIGTSCTNSRLED	368		
Db	294	GQIVISVNETIPNQEMADEVQRASAEKAHYIGEAGTNLKD1KDVQFIGSCTNSRLED	353		
Qy	369	LRAAAAVYKGRRKKAQPKVSKAMVYPSGLVYKTOAEEGGLDKEFAGFWREAGCSMCLGM	428		
Db	354	LRAAAAVYKGRRKKAQDKNVKRLWVPSGLVYKEQAEGGLKIFIAGAEVRNPGLCSMCLGM	413		
Qy	429	NPDLAPQERCCASTNSRNPFPGRQGAGGTHIMSPWMAAAGIVKLADYRKL	481		
Db	414	NDRLGEVERCCASTNSRNPFPGRQGAGGTHIMSPWMAAAGIVKLADYRKL	466		

RESULT 25	LEU2	EC057	STANDARD	PRT;	465 AA.
	ID	LEU2	EC057		
	AC	Q8XA00;			
	DT	15-JUN-2002	(Rel. 41, Created)		
	DT	15-JUN-2002	(Rel. 41, Last sequence update)		
	DT	15-JUN-2002	(Rel. 41, Last annotation update)		
	DE	3-isopropylmalate dehydratase large subunit	(EC 4.2.1.33)		
	DE	(Isopropylmalate isomerase) (Alpha-IPM isomerase)	(IPMI)		
	GN	LEUC	OR 20081	OR EC057.	
	OS	Escherichia coli	O157:H7.		
	OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;			
	OC	Escherichia.			
	OX	NCBI_TaxID:83334;			
	RN				
	RP	SEQUENCE FROM N.A.			
	RC	STRAIN=O157:H7 / EDL933 / ATCC 700927;			
	RX	MEDLINE=1070435; PubMed=11206551;			
	RA	Perna N.T., Plunkett G., III, Burland V., Mau B., Glasner J.D.,			
	RA	Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,			
	RA	Postai G., Hackett J.J., Klink S., Boutin A., Shao Y., Miller L.,			
	RA	Grobbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamoussis K.,			
	RA	Apodaca J., Arantharaman T.S., Lin J., Yen G., Schwartz D.C.,			
	RA	Welch R.A., Blattner F.R.;			
	RT	"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."			
	RL	Nature 409:529-533 (2001).			
	RN	SEQUENCE FROM N.A.			
	RP	STRAIN=O157:H7 / RIMD 0509952;			
	RC	MEDLINE=2115631; PubMed=11258796;			
	RX	Hayashi T.-G., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,			
	RA	Han C.-G., Ohnsubo E., Murata T., Tanaka M., Tobe T.,			

Iida T., Takami H., Honda T., Sasaki C., Ogasawara N., Yasunaga T.,
 Kubara S., Shiba T., Hattori M., Shinohara H.;
 "Complete genome sequence of enterohemorrhagic Escherichia coli
 O157:H7 and genomic comparison with a laboratory strain K-12.";
 DNA Res. 8:1-10 (2001).
 -!- FUNCTION: Catalyzes the isomerization between 2-isopropylmalate
 and 3-isopropylmalate, via the formation of 2-isopropylmaleate.
 -!- CATALYTIC ACTIVITY: 3-isopropylmalate = 2-isopropylmaleate +
 H₂O.
 -!- CATALYTIC ACTIVITY: 2-isopropylmaleate + H₂O = 2-
 isopropylmaleate. Leucine biosynthesis; second step.
 -!- SUBUNIT: Heterodimer of leuC and leuD (By similarity).
 -!- SIMILARITY: BELONGS TO THE ACONITASE/1PM ISOMERASE FAMILY. LEUC
 CC-isopropylmalate subfamily.
 CC- PATHWAY: Leucine biosynthesis; second step.
 CC- PROBOM: P0005184; AAG54376.1; -.
 DR- EMBL: AE005184; BAA23499.1; -.
 DR- EMBL: AP002550; BAA23499.1; -.
 DR- InterPro: IPR001030; Aconitase_N.
 DR- InterPro: IPR004430; LeuC.
 DR- Pfam: PF00330; aconitase; 1.
 DR- PRINTS: PR00415; ACONITASE.
 DR- PROBOM: P000511; Aconitase_N; 1.
 DR- TIGRFAMS: TIGR00170; leuC; 1.
 DR- PROSITE: PS00450; ACONITASE_1; 1.
 DR- PROSITE: PS01244; ACONITASE_2; 1.
 DR- KW- Leucine biosynthesis; lyase; iron-sulfur; 4Fe-4S; Complete proteome.
 INIT MET 0 0 BY SIMILARITY.
 FT- METAL 346 346 IRON-SULFUR (4FE-4S)
 FT- METAL 405 406 IRON-SULFUR (4FE-4S)
 FT- METAL 409 409 IRON-SULFUR (4FE-4S)

Query	Match	Score	Length
Qy	36.2% : OTLIDKVLUQAHYVDEKLGDGVVLLYIDRHTLHEVTSPOAFFFGLRNAGRKRVRPDCTLATTD	1469.5;	465;
Best Local Similarity	61.9% : KTLVQKFLDFRHVVYBAENETPLLYIDRHLVHEVTSPOAFFFGLRAIGRPVRQPKTEATMD	Pred. No. 5	9e-12;
Matches 292;	Conservative 59; Mismatches 112; Indels 9; Gaps		
Db	68 : 61		
Qy	69 : HNVPTTSRKLKDIAFSKEDDSRPFQCVTLLNEVKEFGVITYFGLSDKROGLVHVIGPEQG	128	
Db	62 : HNVSTOT---KDINAC--GEMARQMOELLIKNCKEFGVLYDNLNHPYQG1HVHMGPSEQ	115	
Qy	129 : FTLPGTTVVGDSHTSTHGFAGLAFAFGITSEVEHVLATOLCLITKRSKNNMRQIVDGEELAP	188	
Db	116 : VTLPEMTIVGDSHTATHGFAGLAFAFGITSEVEHVLATOLTLQGAKTMKIEVQGAAAP	175	
Qy	189 : GVSSKDVLHAIGITGAGTGTGAVIEFCGSVIRSLSMEMARMSICNMSIEGGARAGMYAPD	248	
Db	176 : GITADKIVLAAIGKTGAGTGTGAVIEFCGSVIRSLSMEMARMSICNMSIEGGARAGMYAPD	235	
Qy	249 : EITFFYLKGRLPRAKYDPSBWWKATQYWKRNQLQSDPSAKYDIDVFLDAKDITVPTLWTGTS	308	
Db	236 : EITTFYVKGRLHAPK.-GKDFDADAYWKLTQDSEGATFTVTVLQAEISIPOVQVNGTNP	293	
Qy	309 : EDVVPITGVVYDPETFATEAKKADGRRMQLQYMGKLAGTQAEGLDKEEAGFEMREAGCSMCLGM	428	
Db	294 : GQVISVNDNLPDPASADPVERASAEEKALYMGKREGILTEVAIDKVFVGSCTNSRIED	368	
Qy	369 : LRAAAEAVKCRKKKAPNPKSAMVVPQSGLVIKQAEGLDKEEAGFEMREAGCSMCLGM	412	
Db	354 : LRAAAEAIKCRKVAFCVQV--ALVVPESGPVVAQAEAGLDDKIFIEAGFEMREAGCSMCLGM	412	

QY	429	NPDILAPQERCCASTSNRNFFEGROGAGGRHLSPVMAAAGIVKLADWRKL	480
	413	NNDLNPGERCCASTSNRNFFEGROGAGGRHLSPAMAAAAGIVGHFADIRN	464
Db			

Search completed: March 17, 2003, 08:49:29
Job time : 24 secs

